

AMENDMENTS TO THE CLAIMS:

Claim 44 is amended. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-43 (Canceled).

Claim 44 (Currently amended). A variant of a parent Glycoside Hydrolase Family 53 galactanase, comprising an alteration in at least one of the following positions:

90, 91, 181, 303, 305, and 313,

wherein

- (a) the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 80% identical to SEQ ID NO: 1;
- (b) the variant comprises an amino acid sequence which is at least 80% identical and less than 100% identical to SEQ ID NO: 1;
- (c) each position is the number of the corresponding amino acid residue in SEQ ID NO: 1;
- (d) the alteration(s) are independently
 - (i) an insertion of an amino acid immediately downstream of the position,
 - (ii) a deletion of the amino acid which occupies the position, and/or
 - (iii) a substitution of the amino acid which occupies the position with a different amino acid; and
- (e) the variant has galactanase activity.

Claim 45 (Previously presented). The variant of claim 44, wherein the alteration(s) are substitutions.

Claim 46 (Previously presented). The variant of claim 44, wherein the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 85% identical to SEQ ID NO: 1.

Claim 47 (Previously presented). The variant of claim 44, wherein the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 90% identical to SEQ ID NO: 1.

Claim 48 (Previously presented). The variant of claim 44, wherein the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 95% identical to SEQ ID NO: 1.

Claim 49 (Previously presented). The variant of claim 44, wherein the variant comprises an amino acid sequence which is at least 85% identical to SEQ ID NO: 1.

Claim 50 (Previously presented). The variant of claim 44, wherein the variant comprises an amino acid sequence which is at least 90% identical to SEQ ID NO: 1.

Claim 51 (Previously presented). The variant of claim 44, wherein the variant comprises an amino acid sequence which is at least 95% identical to SEQ ID NO: 1.

Claim 52 (Previously presented). The variant of claim 44, which comprises an alteration at position 90.

Claim 53 (Previously presented). The variant of claim 52, wherein the variant comprises:
90A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 54 (Previously presented). The variant of claim 53, wherein the variant comprises:
90A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,T,V,W,Y.

Claim 55 (Previously presented). The variant of claim 44, which comprises an alteration at position 91.

Claim 56 (Previously presented). The variant of claim 55, wherein the variant comprises:
91A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 57 (Previously presented). The variant of claim 44, which comprises an alteration at position 181.

Claim 58 (Previously presented). The variant of claim 57, wherein the variant comprises:
181A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 59 (Previously presented). The variant of claim 44, which comprises an alteration at position 303.

Claim 60 (Previously presented). The variant of claim 59, wherein the variant comprises:
303A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 61 (Previously presented). The variant of claim 44, which comprises an alteration at position 305.

Claim 62 (Previously presented). The variant of claim 61, wherein the variant comprises:
305A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 63 (Previously presented). The variant of claim 44, which comprises an alteration at position 313.

Claim 64 (Previously presented). The variant of claim 63, wherein the variant comprises:
313A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 65 (Previously presented). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

- (a) Y214N,S+N247Y+L306Q; Y214A; F216FVASTG; and/or P89W+W86N;
- (b) A90S+H91D; H91N,L,D; N313D; N303D,H; and/or N305D,H;
- (c) Y22P, N24P, T25P, A29P, A53P, N56P, T93P, D101P, W142P, T147P, Q198P, L203P, S204P, S219P, S258P, S288P, A304P, A311P, Q318P, A322P, S324P, S325P, and/or S327P;
- (d) W107S,H;
- (e) Q126E;
- (f) N39C+L326C; V20C+G320C; Y110C+G163C; W150C+N194C; T274C+V328C; and/or I301C+F316C; and/or

- (g) A90C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
H91A,C,D,E,F,G,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
N181A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;
N303A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;
N305A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y; and/or
N313A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y.

Claim 66 (Previously presented). The variant of claim 65, which is a variant of a *Myceliophthora thermophila* galactanase.

Claim 67 (Previously presented). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

- (a) V20P, V25P, E29P, V41P, V50P, W53P, N56P, T94P, A96P, W142P, L169P, W185P, Q198P, M203P, A219P, A221P, T222P, Q258P, A261P, D262P, S288P, N305P, A311P, A322P, S324P, and/or S325P;
- (b) T113C+G163C, W185C+S229C, S218C+A221C, R227C+V283C; and/or
- (c) A90C,D,E,F,G,H,I,J,K,L,M,N,P,Q,R,S,T,V,W,Y;
H91A,C,D,E,F,G,I,J,K,L,M,N,P,Q,R,S,T,V,W,Y;
N181A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y;
N303A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y;
N305A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y; and/or
N313A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y.

Claim 68 (Previously presented). The variant of claim 67, which is a variant of a *Humicola insolens* galactanase.

Claim 69 (Previously presented). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

- (a) D181N, D181N+S90A+D91H;
- (b) T3P, Y20P, N24P, L25P, T29P, A31P, V50P, S53P, S56P, T93P, T94P, S96P, W142P, L144P, E146P, T147P, T172P, E200P, S203P, A219P, A256P, A258P, S261P, S264P, I266P, T288P, I301P, A304P, Y318P, and/or E324P;
- (c) L13C+L65C, N24C+Q30C, S218C+A221C, A304C+Y318C; and/or

- (d) S90A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,T,V,W,Y;
 D91A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 D181A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 N303A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;
 G305A,C,D,E,F,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; and/or
 N313A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y; and/or
- (e) I9F,Y,W; L12V; L80F; L82Y; F191Y,W; Y213F; I9W+L12V; L82Y+L80F.

Claim 70 (Previously presented). The variant of claim 69, which is a variant of an *Aspergillus aculeatus* galactanase.

Claim 71 (Previously presented). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

- (a) K-6P, S-4P, L-2P, K1P, V20P, S26P, K29P, D31P, A54aP, G54eP, N57P, K93P, A97P, N101P, S171P, S185P, T256P, N260P, N266P, D286P, E288aP, A289P, A302dP, S302yP, Y302zP, A302bbP, E302ccP, E302ggP, F305P, D311P, F318P;
- (b) S18C+Y302qC, G40C+Q330C, V44C+A69C, I48C+A62C, N50C+D84C, G54gC+T302xC, N56C+G302rC, A62C+G146C, K106C+A159C, K114C+A163C, E183C+G221C, T227C+A283C, A234C+V241C, Y250C+Q273C, A302aaC+A302iiC; and/or
- (c) A90C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;
 K91A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y;
 N181A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;
 K303A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y;
 F305A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; and/or
 Q313A,C,D,E,F,G,H,I,K,L,M,N,P,R,S,T,V,W,Y.

Claim 72 (Previously presented). The variant of claim 71, which is a variant of a *Bacillus licheniformis* galactanase.

Claim 73 (Previously presented). The variant of claim 44, wherein the parent galactanase is obtained from a strain of *Aspergillus*, *Bacillus*, *Bifidobacterium*, *Cellvibrio*, *Clostridium*, *Humicola*, *Meripilus*, *Myceliophthora*, *Pseudomonas*, *Thermomyces*, *Thermotoga*, *Xanthomonas*, or *Yersinia*.

Claim 74 (Previously presented). An animal feed composition, comprising a variant of claim 44.

Claim 75 (Previously presented). A method for hydrolyzing lactose, comprising treating the lactose with a galactanase variant of claim 44.